Barley Genetics Newsletter (2012) 42:12-35

REPORTS OF THE COORDINATORS

Overall coordinator's report

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Since the latest overall coordinator's report many barley researchers met at the 11th International Barley Genetics Symposium in Hangzhou, China, April 15 – 20, 2012. About 400 participants attended the meetings, 10 different sessions and 3 workshops were arranged, 61 papers and a number of 100 posters were presented. We could get much information of many interesting papers with new and interesting results for the barley community with fruitful discussions. AS in all previous Symposia a workshop on "Barley Genetic Linkage Groups, Barley Genome and Collections" took place in the evening of April 15th, 2012, in the 'First World Hotel' in Hangzhou. About 50-60 delegates participated and several important topics were discussed very intensively. A report of this workshop is published in this volume BGN 42:1-3.

The most important outcome of this workshop was that the development of genetic markers is emerging so fast that it is impossible for the chromosome coordinators to summarize the enourmous results any more. According to intensive discussions the workshop concluded that the concept of the seven chromosome coordinators is not needed any more. But the coordinators of the collections and barley stocks are more than ever requested for collecting data and keep the material regenerated. Also an extension of coordinators for different important agronomic trait collections was requested by barley breeding people. In this connection I want to take the opportunity to thank all the chromosome coordinators for their immense and tidious work during the years, their efforts writing reports every year, follow up all the published literature with important results and their good coorporation.

The continuation of Barley Genetics Newsletter was also discussed very intensively, and the workshop suggested that it is the best forum and the most important part for barley genetic stock descriptions. It was also requested to publish an updated complete version of the genetic stock descriptions in one volume which will hopefully be presented in this volume.

During the same Symposium another workshop on "Barley Genetic Stocks – Global Use and Potential" took place in the evening of April 18th, 2012 in the 'First World Hotel' in Hangzhou. About 80 delegates participated. This workshop was initiated by the users of Barley Genetic Stocks (BGS) to make recommendations on future directions to the International Organizing Committee (IOC) of the International Barley Genetics Symposium (IBGS). The report of this workshop is published in this volume BGN 42:4-9.

An overview on historic and current activities involving barley genetic stocks was presented as a PowerPoint presentation. After this introduction several speakers were asked to present their opinions of the importance of barley genetic stocks. As key speaker Takao Komatsuda from Japan presented as BGS structure using the six-rowed spike 1 (*vrs1*) gene as an example. Several other speakers from different research centres followed: Nils Stein, Germany, Mats Hansson, Denmark, Michele Stanca, Italy, Pat Hayes, USA, Gary Muehlbauer, USA, Robbie Waugh, Scotland, Morten Rasmussen, Sweden, and Duane Falk, Canada. Every speaker demonstrated in one or the other way how the have been or are using barley genetic stocks in their research projects. All of them stressed the importance of BGS, that the barley community has a joint responsibility to secure BGS and plant genetic resources (PGR) and that a strategy for long term conservation of global BGS must be found not only to secure them but also to access for all information.

Again the to-days status and the future of Barley Genetics Newsletter (BGN) was brought up for discussion. Suggestions were made that it should develop to a Barley Genetic Stock (BGS) newsletter providing mainly BGS descriptions but also open for short research reports. Jerry Franckowiak, Australia, stressed that recommendations should be made to the International Organizing Committee of IBGS to change the format of BGN into a Newsletter with descriptions of BGS and the possibility for short reports. A vote was made where about 20 participants voted for it and no one objected. A proposal will be presented to the IOC.

An important topic was then raised for discussion: the establishment of a 'Barley Genetic Stocks advisory board or committee'. After brief discussion a vote was made where about 15 participants voted for and nobody opposed. Michele Stanca, Italy, a member of the International Organizing Committee (IOC) suggested to put it into a motion for forwarding to IOC.

As last motion Michele Stanca suggested to give a proposal to the International Organizing Committee to integrate the barley genetic stock workshops into the International Barley Genetics Symposium program with the full effort in 2016 at the 12th IBGS in USA. Full support was given by the workshop that he should make this proposal.

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Barley Genetic Stocks Collection
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During the period January 2012 through February 2013 a total of 3,525 accession samples of GSHO (Barley Genetic Stock Accessions) were distributed in a total of 27 separate requests by scientists. One large request (2,873) for the available mapping population lines from the Barley CAP project made up a large quantity of the numbers. These requests were distributed to scientists in Denmark, Germany, Japan, United Arab Emirates, and the U.S.
No new accessions were added during this period.

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Coordinator's report: Translocations and balanced tertiary trisomics

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Farre and colleagues (2012) characterized reciprocal translocation present in a widely grown barley cultivar. Albacete is a barley cultivar widely grown in recent decades in Spain and carrying a reciprocal translocation which obviously does not affect its agronomical fitness. This translocation has been characterized by a combination of cytological and molecular genetic approaches. Recombination frequencies between markers on chromosomes 1H and 3H were estimated to determine the boundaries of the reciprocal interchange. Fine-mapping of the regions around the translocation breakpoints was used to increase the marker density for comparative genomics. The results obtained in this study indicate that the translocation is quite large with breakpoints located on the long arms of chromosomes 1H and 3H, between the pericentromeric (AAG)(5) bands and above the (ACT)(5) interstitial distal bands, resulting in the reciprocal translocation 1HS.1HL-3HL and 3HS.3HL-1HL. The gene content around the translocation breakpoints could be inferred from syntenic relationships observed among different species from the grass family Poaceae (rice, Sorghum and Brachypodium) and was estimated at approximately 1,100 and 710 gene models for 1H and 3H, respectively. Duplicated segments between chromosomes Os01 and Os05 in rice derived from ancestral duplications within the grass family overlap with the translocation breakpoints on chromosomes 1H and 3H in the barley cultivar Albacete (Farre *et al*., 2012).

A novel statistical-genetic approach for the construction of linkage maps in populations obtained from reciprocal translocation heterozygotes of barley was reported. Using standard linkage analysis, translocations usually lead to 'pseudo-linkage': the mixing up of markers from the chromosomes involved in the translocation into a single linkage group. Close to the translocation breakpoints recombination is severely suppressed and, as a consequence, ordering markers in those regions is not feasible. The novel strategy presented is based on (1) disentangling the "pseudo-linkage" using principal coordinate analysis, (2) separating individuals into translocated types and normal types and (3) separating markers into those close to and those more distant from the translocation breakpoints. The methods make use of a consensus map of the species involved. The final product consists of integrated linkage maps of the distal parts of the chromosomes involved in the translocation (Farre *et al*., 2011).

Transcriptional activity of translocated NORs in barley was studied (Kitanova and Georgiev, 2012). The barley cultivar "Freya" and structural mutant forms ab, s, q, T21 and T627 were used to investigate the transcriptional activity of homologous rDNA loci (NORs) based on the positive reactions of NORs of metaphase chromosome with AgNO3 and the number and size of silver stained nucleoli in somatic interphase cells and meiocytes. The chromosomal rearrangement enables testing of intrachromosomal suppression of NORs and provides insight into the mechanisms of intraspecific nucleolar dominance. Considerable difference in gene expression (nucleolar dominance) after AgNO3 and FISH was established only in line ab, when both NORs (5H and 6H rDNA loci) are co-localized on the same or opposite arms of the chromosome. Translocation-induced intraspecific nucleolar dominance is probably the result of interaction of NOR6H and NOR5H or other genetic factors (like up-elements) located on the NOR-bearing chromosomes.

Joshi and colleagues (2011) used gametocidal (Gc) chromosomes 2C and 3C(SAT) to dissect barley 2H added to common wheat. The authors selected plants carrying structurally rearranged aberrant 2H chromosomes and characterized them by sequential C-banding and in situ hybridization. 66 dissection lines were identified of common wheat carrying single aberrant 2H chromosomes. The aberrant 2H chromosomes were of either deletion or translocation or complicated structural change. Their breakpoints were distributed in the short arm (2HS), centromere (2HC) and the long arm (2HL) at a rough 2HS/2HC/2HL ratio of 2:1:2. PCR analysis was conducted of the 66 dissection lines using 115 EST markers specific to chromosome 2H. Based on the PCR result a physical or cytological map of chromosome 2H that were divided into 34 regions separated by the breakpoints of the aberrant 2H chromosomes. Forty-seven markers were present in 2HS and 68 in 2HL. The 2H cytological map was compared with a previously reported 2H genetic map using 44 markers that were used in common to construct both maps. The order of markers in the distal region was the same on both maps but that in the proximal region was somewhat contradictory between the two maps. It was found that the markers distributed rather evenly in the genetic map were actually concentrated in the distal regions of both arms as revealed by the cytological map. We also recognized an EST-marker or gene-rich region in the 2HL interstitial region slightly to the telomere (Joshi *et al*., 2011).

A spontaneous interspecific Robertsonian translocation was revealed by GISH in the progenies of a monosomic 7H addition line originating from a new wheat 'Asakaze komugi' x barley 'Manas' hybrid. FISH with repetitive DNA sequences (Afa family, pSc119.2, and pTa71) allowed identification of all wheat chromosomes, including wheat chromosome arm 4BS involved in the translocation. FISH using barley telomere- and centromere-specific repetitive DNA probes (HvT01 and (AGGGAG)(n)) confirmed that one of the arms of barley chromosome 7H was involved in the translocation. Simple sequence repeat (SSR) markers specific to the long (L) and short (S) arms of barley chromosome 7H identified the translocated chromosome segment as 7HL. Further analysis of the translocation chromosome clarified the physical position of genetically mapped SSRs within 7H, with a special focus on its centromeric region. The presence of the HvCslF6 gene, responsible for (1,3;1,4)-beta-D-glucan production, was revealed in the centromeric region of 7HL. An increased (1,3;1,4)-beta-D-glucan level was also detected in the translocation line, demonstrating that the HvCslF6 gene is of potential relevance for the manipulation of wheat (1,3;1,4)-beta-D-glucan levels (Cseh *et al*., 2011).

The collection is being maintained in cold storage. To the best knowledge of the coordinator, there are no new publications dealing with balanced tertiary trisomics in barley. Limited seed samples are available at any time, and requests can be made to the coordinator.

References:

Cseh, A., K. Kruppa, I. Molnar, M. Rakszegi, J. Dolezel, and M. Molnar-Lang. 2011. Characterization of a new 4BS.7HL wheat-barley translocation line using GISH, FISH, and SSR markers and its effect on the beta-glucan content of wheat. Genome 54: 795-804.

Farre, A., I.L. Benito, L. Cistue, J.H. de Jong, L. Romagosa, and J. Jansen. 2011. Linkage map construction involving a reciprocal translocation. Theoretical and Applied Genetics 122:1029-1037.

Farre, A., A. Cuadrado, L. Lacasa-Benito, L. Cistue, L. Schubert, J. Comadran, J. Jansen, and L. Romagosa. 2012. Genetic characterization of a reciprocal translocation present in a widely grown barley variety. Mol Breed 30:1109-1119.

Joshi, G.P., S. Nasuda, and T.R. Endo. 2011. Dissection and cytological mapping of barley chromosome 2H in the genetic background of common wheat. Genes Genet Syst 86: 231-248.

Kitanova, M. and S. Georgiev. 2012. Transcriptional Activity of Translocated Nors in Barley (Hordeum vulgare L.). Biotechnol Biotec Eq 26**.** 2855-2865.

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Coordinator's Report: Desynaptic Genes.

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The coordinator for Desynaptic Genes, Andreas Houben, Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, asked me to summarize the status of this genetic stock collection.

15 localized Desynaptic Genes (des) exist and they are described in Barley Genetic Newsletter (BGN) Volume 26 (1997), some of them are updated in BGN 41 by J.D. Franckowiak. All of them have assigned GSHO numbers, are incorporated and available at the USDA-ARS. National Small Grains Germplasm Research Facility, Aberdeen, ID 83210, USA. They are summarized in Table 1.

Table1.

Mutant name	Symbol with allele	BGS description	GSHO number
Desynapsis 1	des1.a	12	592
Desynapsis 2	des2.b	119	593
Desynapsis 3	des3.c	386	594
Desynapsis 4	des4.d	13	595
Desynapsis 5	des5.e	14	596
Desynapsis 6	des6.i	215	597
Desynapsis 7	des7.j	64	598
Desynapsis 8	des8.k	387	599
Desynapsis 9	des9.n	388	600
Desynapsis 10	des10.p	389	601
Desynapsis 11	des11.r	390	602
Desynapsis 12	des12.s	391	603
Desynapsis 13	des13.t	392	604
Desynapsis 14	des14.u	393	605
Desynapsis 15	des15.x	394	606

In the mid 1980s an extensive backcrossing program was initiated by J.D. Franckowiak, USA, now working as senior breeder in Australia, to introgress mutated loci from the worldwide barley

collection of morphological and developmental mutants into a common genetic background, he used the cultivar 'Bowman', a high-yielding with good brewing properties cultivar of the Midwest of USA at that time. Also all the 15 localized Desynapsis genes, in some cases more than 1 allele of the locus plus 2 unlocalized genes were backcrossed to Bowman and near-isogenic backcrossed Bowman lines (BW) were produced. All these lines were regenerated during 2010 and 2011 in the glasshouse of the Department of Genetics, Lund University, Sweden. They are incorporated and stored at Nordgen (Nordic Genetic Resource Center) Alnarp, Sweden, and seeds are available at any time. In Table 2 all existing BW lines are listed with the BW and NGB numbers, but no GSHO numbers are assigned and not available at USDA-ARS.

Table 2.

Mutant name	Symbol with allele	BW number	NGB Number
Desynapsis 1	des1.a	228	22055
Desynapsis 1	des1.v	229	22056
Desynapsis 2	des2.b	238	22065
Desynapsis 3	des3.c	239	22066
Desynapsis 4	des4.d	241	22068
Desynapsis 4	des4.af	240	22067
Desynapsis 4	des4.h	242	22069
Desynapsis 5	des5.e	243	22740
Desynapsis 6	des6.i	244	22070
Desynapsis 6	des6.o	245	22071
Desynapsis 7	des7.j	246	22072
Desynapsis 8	des8.k	247	22073
Desynapsis 8	des8.l	248	22471
Desynapsis 9	des9.n	249	22074
Desynapsis 10	des10.p	230	22057
Desynapsis 11	des11.r	231	22058
Desynapsis 12	des12.s	232	22059
Desynapsis 12	des12,w	233	22060
Desynapsis 13	des13.t	234	22061
Desynapsis 14	des14.u	235	22062
Desynapsis 15	des15.x	236	22063
Desynapsis 15	des15.y	237	22064
Desynapsis.aj	des.aj	226	22053
Desynapsis.ak	des.ak	227	22054

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Coordinator´s Report: Disease and Pest Resistance Genes

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In the table below you will find papers published in 2011/2012 extending last year´s list of information available on molecular markers for major resistance genes in barley published in Barley Genetics Newsletter 41.

List of papers published on mapped major resistance genes in barley updated until October 31. 2012.

Resistance gene	**Chromosomal location**	**Reference**
Magnaporthe oryzae		
Rmo2	7H	Nga et al. 2012
Puccinia hordei		
Lr-APR	5HS	Liu et al. 2011
$Rph_{MBR1012}$	1HS	Koenig et al. 2012
Rph20	5HS	Hickey et al. 2012
Rph21	4H	Sandhu et al. 2012
Pyrenophora teres* f. *teres		
N.N.	6H	Gupta et al. 2011
Rhynchosporium commune		
Rrs2	7HS	Fu 2012
Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV)		
rym4, rym5	3HL	Hofinger et al. 2011
Rym17	3H	Kai et al. 2012
rym18	4H	Kai et al. 2012

References:

Fu, Y.B. 2012 Population-based resequencing analysis of wild and cultivated barley revealed weak domestication signal of selection and bottleneck in the *Rrs2* scald resistance gene region. Genome 55: 93-104.

Gupta, S., R. Loughmann, M. Cakir, S. Westcott, and R. Lance. 2011. Identifying genetic complexity of 6H locus in barley conferring resistance to *Pyrenophora teres* f. *teres*. Plant Breeding 130:423-429.

Hickey, L.T., W. Lawson, G.J. Platz, M. Dieters, and J. Franckowiak. 2012. Origin of leaf rust adult plant resistance gene *Rph20* in barley. Genome 55:369-399.

Hofinger, B.J., J.R.Russel, C.G. Bass, T. Baldwin, M. Dos Reis,, P.E. Hedley, Y.D. Li, M. Macaulay, R. Waugh, K.E. Hommond-Kosack, and K. Kanyuka. 2011. An exceptional high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. Mol. Ecology 20:3653-3668.

Kai, H., K. Takata, M. Tsukazaki, M. Furusho, and T. Baba. 2012. Molecular mapping of *Rym17*, a dominant and *rym18* a recessive barley yellow mosaic virus (BaYMV) resistance genes derived from *H. vulgare*. Theor Appl Genet 124:577-583.

König, J., D. Kopahnke, B.J. Steffenson, N. Przulj, T. Romeis, M.S. Röder, F. Ordon, and D. Perovic. 2012. Genetic mapping of a leaf rust resistance gene in the former Yugoslavian landrace MBR1012. Mol. Breeding 30:1253-1264.

Liu, F., S. Gupta, X.Q. Zhang, M. Jones, R. Loughman, R. Lance, and C. Li. 2011. PCR markers for selection of adult plant leaf rust resistance in barley (*Hordeum vulgare* L.). Mol Breeding 28: 657-666.

Nga, N.T.T., Y. Inoue, I. Chuma, G.S. Hyon, K. Okada, T.T.P. Vy, M. Kusaba, and Y. Tosa. 2012. Identification of a novel locus *Rmo2* conditioning resistance in barley to host specific subgroups of *Magnaporthe oryzae*. Phytopathology 102: 674-682.

Sandhu, K.S., K.L. Forrest, S. Kong, U.K. Bansal, D. Singh, M.J. Hayden, and R.F. Park. 2012. Inheritance and molecular mapping of a gene conferring seedling resistance against *Puccinia hordei* in the barley cultivar Ricardo. Theor Appl Genet 125:1403-1411.

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Coordinator's report: *Eceriferum* genes

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Presence of the wax coating and its composition is an important feature of the barley plant. It reduces evaporation of water from the plant and helps protect it against pathogens. The waxless *Eceriferum* mutants affect the presence and type of epicuticular waxes on the different organs. Many different surface wax mutants have been isolated as induced or spontaneous mutants. All 79 defined loci are published as descriptions in Barley Genetics Newsletter (BGN) 26 and later. They are valid and up-to-date.

All the 79 gene loci have been backcrossed to a common genetic background, the cultivar 'Bowman' by J.D. Franckowiak, Australia. They are available as Near Isogenic Lines (NIL) at the Nordic Genetic Resource Center (Nordgen), Sweden, www.nordgen.org and at the Small Grain Germplasm Research Facility (USDA–ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov.

Single Nucleotide Polymorphism (SNP) genotyping provide a detailed understanding of the genetic composition of the barley genome by using the above mentioned Near Isogenic Lines (NIL) (*Druka et al*., 2011).

Chao Li et al. (2013) reported that *Eceriferum* locus *zv* (*cer-zv*) is located in a pericentromeric region on chromosome 4H. They used the *cer-zv.268* allele where the surface wax coating on the spike, leaf sheath and stem, and leaf blade appears absent, plants are semidwarf and the hull is poorly attached to the seed. It is also sensitive to drought. The leaves showed increased permeability to ethanol and toluidine blue dye, and there was a reduction in four major cutin monomers, but no reduction in wax loads was found. The results indicate that the *cer-zv* mutant is associated with a defect in cutins which might be responsible for the increased transpiration rate and drought sensitivity.

References:

Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010, Genetic Dissection of barley morphology and development. Plant Physiology 155:617-627.

Chao, Li, Aldong Wang, Xiaoying Ma, Mohammad Pourkheirandish, Shun Sakuma, Ning Wang, Shunzong Ning, Eviatar Nevo, Christiane Nawrath, Takao Komatsuda, and Guoxiong Chen. 2013. An *eceriferum* locus, *cer-zv*, is associated with a defect in cutin responsible for water retention in barley (*Hordeum vulgare*) leaves. Theor Appl Gentic 2013 Mar; 126(3):637-646.

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Coordinator's report: Nuclear genes affecting the chloroplast

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Barley chlorophyll mutants have been named *albina*, *xantha*, *viridis*, *chlorina*, *tigrina* and *striata* depending on their colour and colour pattern. In the *albina* mutants the leaves are completely white due to lack of both chlorophyll and carotene pigments. The *xantha* mutants are yellow and produce carotene, but no chlorophyll. The *chlorina* and *viridis* mutants are both pale green, but differ in *chlorina* being viable. The *tigrina* and *striata* mutants are stripped transverse and along the leaves, respectively.

Mueller *et al*. (2012) studied the barley chlorina mutants *fch2* and *clo-f2*, which comprise an allelic group of 14 different lines. They are characterized by a reduced amount or total lack of chlorophyll *b*. Absence of chlorophyll *b* results in an aberrant composition of the light-harvesting apparatus, which is the reason why many studies have been conducted with this group of mutants. However, not until now the identity of the *fch2* locus has been described. In their study, the authors review the historic naming of the 14 mutants and how they now should be named according to the present nomenclature rules. It was found that the *fch2* gene encodes the chlorophyllide *a* oxygenase, which catalyses the oxidation of the 7-methyl group of chlorophyllide *a* to the 7-formyl group of chlorophyllide *b*. No chlorophyll *b* could be detected in lines carrying mutations leading to premature stop of translation or in two missense mutants. Six other missense mutants showed detectable amounts of chlorophyll b.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter issue 37 (2007): 37-43 and is also linked from
http://www.carlsberglab.dk/professors/Hansson/Pages/default.aspx

New reference:

Mueller, A. H., C. Dockter, S. P. Gough, U. Lundqvist, D. von Wettstein, and M. Hansson. 2012. Characterization of mutations in barley *fch2* encoding chlorophyllide *a* oxygenase. Plant Cell Physiol. 53:1232-1246.

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Coordinator's report: Early maturity and Praematurum genes

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The demand for early maturity has grown for several decades and became an important goal for plant breeding. Time to flowering has an important impact on yield and has been a key trait in the domestication of crop plants. Early maturity material has been collected for different geographic regions and climate conditions, today a critical issue in times of global warming. Many different early maturity or Praematurum mutants collected in different parts of the wold are incorporated in Genebanks. Only in Scandinavia more than 1000 such mutants have been isolated, their phenotypes have been described, analysed genetically and used in plant breeding world wide. Several early maturity or Praematurum loci have been identified among them also day-length neutral ones. In the last coordinator's report in Volume 41 (2011) it became reported by Zakhrabekova, S. et al. (2012) that the famous *mat-a* (*eam8*) gene with its photoperiod insensitivity got identified as a homolog of the *Arabidopsis thaliana* circadian clock regulator *Early flowering 3* (*Elf3*) by characterizing 87 induced mat-a mutant lines.

Faure *et al*. (2012) showed several months later that commercial barley cultivars bred for short growing seasons by use of *early maturity 8* (*eam8*) mutations also termed *mat-a* are severely compromised in clock gene expression and clock outputs. They identified *EAM8* at a barley ortholog of the *Arabidopsis thaliana* circadian clock regulator *EARLY FLOWERING 3* (*ELF3*). They also showed that *eam8* mutants have increased expression of the floral activator *HvFT1* which is independent of allelic variation at *Ppd-H1*.

Comadran et al. (2012) reported for one genetically divergent region the identification of a natural variant of the barley homolog of *Antirrhinum CENTRORADIALIS* (*HvCEN*) as a contributor to successful environmental adaptation. The distribution of the *CEN* alleles in a large collection of wild and landraces accessions as well as induced early maturity mutants indicates that this involved selection and enrichment of pre-existing genetic variants rather than the acquisition of mutations after domestication. In order to prove this natural variation of *HvCEN* was responsible for the observed variation in flowering time they exploited the historical Swedish barley Early maturity mutant collection of *Praematurum-c* (*mat-c*). They examined 29 *mat-c* mutants that flowered earlier than their mother cultivars. The mutants showed different constitutions and from these results they concluded that variation in *HvCEN* was important in enabling geographic range extension.

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Coordinator's report: ear morphology genes

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Barley is one of the most important cereal crops which ranks fourth in terms of production and cultivation all over the world. It is a model organism for genetic and genomic studies in Triticeae, due to the high degree of natural variation and wide adaptability, the diploid genome structure and the strongly inbreeding-based mating system, as well as the wide array of genetic and genomic resources. Wide genetic variations for developmental traits have been observed in barley and this peculiarity is believed one of the main evolutionary driving force for its broad adaptability. It is diploid with a large haploid genome of 5.1 giga bases (Gb). Recently Mayer *et al* (2012) presented an integrated and ordered physical, genetic and functional sequence resource that describes the barley gene-space in a structured whole genome context. A physical map of 4.98 Gb, with more than 3.90 Gb anchored to a high-resolution genetic map has been developed. Projecting a deep whole-genome shotgun assembly, complementary DNA and deep RNA sequence data onto this framework supports 79,379 transcript clusters, including 26,159 'high-confidence' genes with homology support from other plant genomes.

Abundant alternative splicing, premature termination codons and novel transcriptionally active regions suggest that post-transcriptional processing forms an important regulatory layer. Survey sequences from diverse accessions reveal a landscape of extensive single-nucleotide variation. These data provide a platform for both genome-assisted research and enabling contemporary crop improvement.

Attention is mainly focused on the morphological mutants of barley spike, which affect the phytomeric structure of the rachis (long/short internode, branched), florets (two-rowed/six-rowed, multiflorus, reduced lateral spikelets, deficiens, laxatum), lemma (leafy lemma), glumes (third outer glumes, wider outer glumes), awns (awnless, short awns, triple awned, long awned glumes, branched long awned glumes, calcaroides, Hooded, elevated hooded, seeded in hood), grains (colorless/colored grain, naked/hulled grain, waxy), timing of flowering. A new Hooded mutant has been observed in rare out crosses of the extra flower in the Hood, named "Seeded in Hood", in which small seed in some Hood is developed. This mutant generated a complex

segregant population from which several Hooded double mutants have been isolated. Genetic studies are in progress to define the segregation of the F2 derived by the cross "Seeded in Hood" x Cometa (two-rowed commercial cultivar). Most of these mutants, behind the morphological and genetic studies, will provide breeders with original materials for pre-breeding work (Stanca *et al* 2013).

The timing of flowering during the year is an important adaptive trait that strongly influences reproductive fitness and has been deeply studied by Faure *et al* (2012). The circadian clock is an autonomous oscillator that produces endogenous biological rhythms with a period of about 24 h. This clock allows organisms to coordinate their metabolism and development with predicted daily and seasonal changes of the environment. In plants, circadian rhythms contribute to both evolutionary fitness and agricultural productivity. Nevertheless, it has been shown that commercial barley cultivars bred for short growing seasons by use of early maturity 8 (*eam8*) mutations, also termed mat-a, are severely compromised in clock gene expression and clock outputs. EAM8 has been identified as a barley ortholog of the Arabidopsis thaliana circadian clock regulator EARLY FLOWERING3 (ELF3) and demonstrated that *eam8* accelerates the transition from vegetative to reproductive growth and inflorescence development. It has been proposed that *eam8* was selected as barley cultivation moved to high-latitude short-season environments in Europe because it allowed rapid flowering in genetic backgrounds that contained a previously selected late-flowering mutation of the photoperiod response gene *Ppd-H1*. *eam8* mutants have been shown to have increased expression of the floral activator HvFT1, which is independent of allelic variation at *Ppd-H1*. The selection of independent *eam8* mutations shows that this strategy facilitates short growth-season adaptation and expansion of the geographic range of barley, despite the pronounced clock defect.

A second paper on this subject has been published by Zakhrabekova *et al* (2012) in which the genetics of early maturing cultivar -Mari- has been described. In 1961, the cultivar Mari (*mat-a.8*) was the very first induced early barley (Hordeum vulgare L.) mutant to be released into commercial production. Mari extended the range of two-row spring barley cultivation as a result of its photoperiod insensitivity.

Since its release, Mari or its derivatives have been used extensively across the world to facilitate short-season adaptation and further geographic range extension. By exploiting an extended historical collection of early-flowering mutants of barley, Praematurum-a (*Mat-a*) has been identified, the gene responsible for this key adaptive phenotype, as a homolog of the Arabidopsis thaliana circadian clock regulator Early Flowering 3 (Elf3). 87 induced *mat-a* mutant lines have been characterized and identified >20 different *mat-a* alleles that had clear mutations leading to a defective putative ELF3 protein. Expression analysis of HvElf3 and Gigantea in mutant and wild-type plants demonstrated that *mat-a* mutations disturb the flowering pathway, leading to the early phenotype.

Alleles of Mat-a therefore have important and demonstrated breeding value in barley but probably also in many other day length-sensitive crop plants, where they may tune adaptation to different geographic regions and climatic conditions, a critical issue in times of global warming.

Spring-sown crops that flowered without the need for an extended period of cold to promote flowering and day length–insensitive crops able to exploit the longer, cooler days of higher latitudes emerged and became established. To investigate the genetic consequences of adaptation to these new environments, Comadran *et al* (2012) identified signatures of divergent selection in the highly differentiated modern-day spring and winter barleys. In one genetically divergent region, they identify a natural variant of the barley homolog of Antirrhinum CENTRORADIALIS**2** (HvCEN) as a contributor to successful environmental adaptation. The distribution of HvCEN alleles in a large collection of wild and landrace accessions indicates that this involved selection and enrichment of preexisting genetic variants rather than the acquisition of mutations after domestication.

Spike density in barley is under the control of several major genes, as documented previously by genetic analysis of a number of morphological mutants. One such class of mutants affects the rachis internode length leading to dense or compact spikes and the underlying genes were designated dense spike (*dsp*). Two introgressed genomic segments on chromosome 3H (21SNP loci, 35.5 cM) and 7H (17 SNP loci, 20.34 cM) inBW265, a BC7F3 near isogenic line (NIL) of cv. Bowman as potentially containing the dense spike mutant locus *dsp.ar*, by genotyping 1,536 single nucleotide polymorphism (SNP) markers in both BW265 and its recurrent parent have been delimited. Shainnia *et al* (2012) allocated the gene by high resolution bi-parental mapping to a 0.37 cM interval between markers SC57808 (Hv_SPL14)– CAPSK06413 residing on the short and long arm at the genetic centromere of chromosome 7H, respectively. This region putatively contains more than 800 genes as deduced by comparison with the collinear regions of barley, rice, sorghum and Brachypodium. Classical map-based isolation of the gene *dsp.ar* thus will be complicated due to the infavorable relationship of genetic to physical distances at the target locus.

The awn, an apical extension from the lemma of the spikelet, plays important roles in seed dispersal, burial, and photosynthesis. Barley typically has long awns, but short-awn variants exist. The short awn 2 (*lks2*) gene, which produces awns about 50% shorter than normal, is a natural variant that is restricted to Eastern Asia. Positional cloning revealed that Lks2 encodes a SHI-family transcription factor. Allelism tests showed that *lks2* is allelic to unbranched style 4 (*ubs4*) and breviaristatum-d (*ari-d*), for which the phenotypes are very short awn and sparse stigma hairs. The gene identity was validated by 25 mutant alleles with lesions in the Lks2 gene. Of these, 17 affected either or both conserved regions: the zinc-binding RING-finger motif and the IGGH domain. Lks2 is highly expressed in awns and pistils. Histological observations of longitudinal awn sections showed that the *lks2* short-awn phenotype resulted from reduced cell number. Natural variants of lks2 were classified into three types, but all shared a single-nucleotide polymorphism (SNP) that causes a proline-to-leucine change at position 245 in the IGGH domain. All three lks2 natural variants were regarded as weak alleles because their awn and pistil phenotypes are mild compared with those of the 25 mutant alleles. Natural variants of *lks2* found in the east of China and the Himalayas had considerably different sequences in the regions flanking the critical SNP, suggesting independent origins. The available results suggest that the *lks2* allele might have a selective advantage in the adaptation of barley to high-precipitation areas of Eastern Asia (Yuo *et al* 2012).

A typical barley (*Hordeum vulgare*) floret consists of reproductive organs three stamens and a pistil,and non-reproductive organs — lodicules and two floral bracts, abaxial called 'lemma' and adaxial 'palea'. The floret is subtended by two additional bracts called outer or empty glumes. Together these organs form the basic structural unit of the grass inflorescence, a spikelet. There are commonly three spikelets at each rachis (floral stem of the barley spike) node, one central and two lateral spikelets. Rare naturally occurring or induced phenotypic variants that contain a third bract subtending the central spikelets have been described in barley. The gene responsible for this phenotype was called the THIRD OUTER GLUME1 (*trd1*). The *trd1* mutants fail to suppress bract growth and as a result produce leaf-like structures that subtend each rachis node in the basal portion of the spike. Also, floral development at the collar is not always suppressed.

In rice and maize, recessive mutations in NECKLEAF1 (Nl1) and TASSEL SHEATH1 (Tsh1)genes, respectively, have been shown to be responsible for orthologous phenotypes. Fine mapping of the trd1 phenotype in an F3 recombinant population enabled us to position *trd1* on the long arm of chromosome 1H to a 10 cM region. Houston *et al* (2012) anchored this to a conserved syntenic region on rice chromosome Os05 and selected a set of candidate genes for validation by resequencing PCR amplicons from a series of independent mutant alleles. This analysis revealed that a GATA transcription factor, recently proposed to be *trd1*, contained mutations in 10 out of 14 independent trd1 mutant alleles that would generate nonfunctional TRD1 proteins. Together with genetic linkage data, we confirm the identity of Trd1 as the GATA transcription factor ortholog of rice Nl1 and maize Tsh1 genes.

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Coordinator's report: Semidwarf genes

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Mutants at the praematurum-c (*mat-c*) locus were shown to affect both plant maturity and plant height (Comadran *et al*., 2012). They were also shown to be allelic at the early maturity 6 (*Eam6*) or QTL earliness per se 2S (*eps2S*) locus, which is associated with earlier heading in six-rowed winter and spring barley cultivars. In the population studied, the *eps2S* gene decreased time to flowering and increased yield and thousand kernel weight. Comadran *et al*. (2012) demonstrated that *Eam6.h* and most *mat-c* mutants were caused by DNA sequence changes in the *HvCEN* gene, a homeolog of the *CENTRORADIALIS* (*CEN*) gene in *Antirrhinum*. The early variant at the *Eam6* locus (*Eam6.h* or haplotype II) was shown to have evolved before domestication of barley.

Gain of function (GoF) mutants at the DELLA loci in wheat cause decreased sensitivity to gibberellic acid (GA) and reduced plant height. These reduced height (*Rht-B1b* and *Rht-D1b*) genes in wheat facilitated the 'Green Revolution' and altered foliar disease responses (Saville *et al*., 2012). Mutants at the DELLA locus in barley are described as mutants at the slender 1(*sln1*) locus that cause GoF and loss of function (LoF) (Chandler *et al*., 2002). Saville *et al*. (2012) reported that the GoF mutant *Sln1.d* increased susceptibility to powdery mildew (*Blumeria graminis* f. sp. *hordei*) while the LoF mutant *sln1.c* prevented successful infection. The differences were attributed to host cell death in attempted infection by spores. The GoF mutant was more susceptible to *Ramularia collo-cygni* than the LoF mutant. In contrast to the response to biotropic fungi, the GoF mutant was more resistant to the necrotropic fungus *Oculimacula acuformis* (eyespot) while the LoF mutant was more susceptible.

Changes in protein abundance in juvenile plants were studied in lines differing for the *sdw1*/*denso* dwarfing gene (Kuczyńska *et al*., 2012). Of the 31 protein spots showing differences, functional annotations were identified for 27. Many of them are involved in defence/disease related processes. In an earlier report, Kuczyńska and Wyka (2011) described the effects of the *sdw1/denso* gene on tissues and cells. Leaves and epidermal cells in fully mature leaves were smaller suggesting restricted cell production and cellular growth.

Mutants at the *sdw1* locus were shown to be orthologues of the rice *sd1* gene, which encodes a GA-oxidase that reduces levels of GA and cause the dwarf phenotype (Jai *et al*., 2009). The gibberellin 20-oxidase gene (*Hv20ox2*) was identified as the candidate gene for *sdw1* (Jai *et al*., 2009; 2011). Reduced expression of *Hv20ox2* increased the number of effective tillers and enhanced grain yield. Jia *et al*. (2011) showed that the reduction in *Hv20ox2* levels was 4-fold in the *sdw1.d* or *denso* mutant and 60-fold in the *sdw1.a* (Jotun) mutant. This result could be

explained previous observed differences among *sdw1* mutants in their phenotypic effects and their usefulness in developing barley cultivars.

Pasam *et al*. (2012) reported on mapping of traits in barley using genome-wide association studies (GWAS) based on linkage disequilibrium (LD) for 224 spring barley accessions from a world collection. The panel accessions was genotyped with a customized oligonucleotide pool assay containing 1536 SNPs using Illumina's GoldenGate technology resulting in 957 successful SNPs covering all chromosomes. Plant height was significantly associated with 32 markers located in 19 regions of the genome. The strongest association was with markers in 6HS, followed by the *Eam6*/*eps2S* region of 2HS and the *uzu1* region of 3HL. Other significant plant height associations with likely candidate loci were *Eam1*/*PpdH1* in 2HS, *vrs1* in were 2HL, *sdw1*/*denso* in 3HL, and *Eam5*/*Vrn1*/*Sgh2* in 5HL.

Local cultivars and semi-dwarf cultivars from the ICARDA barley program were evaluated in Ethiopia over several environments by Zerihun (2012). The shorter cultivars, which were more resistant to lodging over environments, had higher average yields than local cultivars. However, the advantages were not recorded in certain environments where shoot fly and water logged soil were production problems. Zerihun (2102) reposted that the late maturity of ICARDA lines would strict acceptance by local farmers. Based on analysis of a doubled haploid population, one of the dwarfing genes in the ICARDA lines is likely located on chromosome 6HS near DArT marker bPb-6002 (Negeri, 2009).

Using doubled haploid lines from the cross between a six-rowed Spanish landrace with a low vernalization requirement and a two-rowed spring German cultivar, Ponce-Molina *et al*. (2012) reported that quantitative trait loci were detected for growth habit, heading date, plant height, and individual grain weight in the region 3HL where the *sdw1*/*denso* gene is located. The population demonstrated that short stature can be combined with early heading date in six-rowed barley.

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